



033267-021.ST25

SEQUENCE LISTING

<110> Schmaljohn, Connie S.  
Fuller, James T.

<120> Nucleic Acid Immunization

<130> 033267-021

<140> US 10/411,205

<141> 2003-04-11

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<212> DNA

<213> Artificial Sequence

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<223> synthetic oligonucleotides which comprise CpG  
motifs

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<221> CDS

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ttattaattt caatataata taaatttaat tttatacaaa aaggagaacg tat atg 176  
Met  
1

aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata tta 224  
Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile Leu  
5 10 15

gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa cag	272
Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys Gln	
20 25 30	
gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta cta	320
Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu	
35 40 45	
gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt acc	368
Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr	
50 55 60 65	
tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa aat	416
Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn	
70 75 80	
att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga ttt	464
Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe	
85 90 95	
atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct gat	512
Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp	
100 105 110	
aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa gct	560
Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys Ala	
115 120 125	
tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa ata	608
Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln Ile	
130 135 140 145	
aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat ttc	656
Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp Phe	
150 155 160	
aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct agt	704
Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser Ser	
165 170 175	
gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca aga	752
Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser Arg	
180 185 190	
aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac aat	800
Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp Asn	
195 200 205	
gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat gtc	848
Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp Val	
210 215 220 225	
aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat gaa	896
Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His Glu	
230 235 240	
aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc acg	944
Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser Thr	

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gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att gat Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile Asp 260 265 270			992
aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat ccg Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr Pro 275 280 285			1040
att gta cat gta gat atg gag aat att att ctc tca aaa aat gag gat Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu Asp 290 295 300 305			1088
caa tcc aca cag aat act gat agt gaa acg aga aca ata agt aaa aat Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys Asn 310 315 320			1136
act tct aca agt agg aca cat act agt gaa gta cat gga aat gca gaa Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala Glu 325 330 335			1184
gtg cat gcg tcg ttc ttt gat att ggt ggg agt gta tct gca gga ttt Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly Phe 340 345 350			1232
agt aat tcg aat tca agt acg gtc gca att gat cat tca cta tct cta Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser Leu 355 360 365			1280
gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct gat Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala Asp 370 375 380 385			1328
aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg gct Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr Ala 390 395 400			1376
cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa aat Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys Asn 405 410 415			1424
caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa ata Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln Ile 420 425 430			1472
ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc gca Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile Ala 435 440 445			1520
tta aat gca caa gac gat ttc agt tct act cca att aca atg aat tac Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn Tyr 450 455 460 465			1568
aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat acg Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp Thr 470 475 480			1616
gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga aga			1664

Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu	Asn	Gly	Arg		
			485					490					495				
gtg	agg	gtg	gat	aca	ggc	tcg	aac	tgg	agt	gaa	gtg	tta	ccg	caa	att	1712	
Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu	Pro	Gln	Ile		
		500					505					510					
caa	gaa	aca	act	gca	cgt	atc	att	ttt	aat	gga	aaa	gat	tta	aat	ctg	1760	
Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp	Leu	Asn	Leu		
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gta	gaa	agg	cgg	ata	gcg	gcg	gtt	aat	cct	agt	gat	cca	tta	gaa	acg	1808	
Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro	Leu	Glu	Thr		
		530				535				540					545		
act	aaa	ccg	gat	atg	aca	tta	aaa	gaa	gcc	ctt	aaa	ata	gca	ttt	gga	1856	
Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	Ile	Ala	Phe	Gly		
				550					555						560		
ttt	aac	gaa	ccg	aat	gga	aac	tta	caa	tat	caa	ggg	aaa	gac	ata	acc	1904	
Phe	Asn	Glu	Pro	Asn	Gly	Asn	Leu	Gln	Tyr	Gln	Gly	Lys	Asp	Ile	Thr		
			565				570							575			
gaa	ttt	gat	ttt	aat	ttc	gat	caa	caa	aca	tct	caa	aat	atc	aag	aat	1952	
Glu	Phe	Asp	Phe	Asn	Phe	Asp	Gln	Gln	Thr	Ser	Gln	Asn	Ile	Lys	Asn		
		580					585						590				
cag	tta	gcg	gaa	tta	aac	gca	act	aac	ata	tat	act	gta	tta	gat	aaa	2000	
Gln	Leu	Ala	Glu	Leu	Asn	Ala	Thr	Asn	Ile	Tyr	Thr	Val	Leu	Asp	Lys		
		595				600						605					
atc	aaa	tta	aat	gca	aaa	atg	aat	att	tta	ata	aga	gat	aaa	cgt	ttt	2048	
Ile	Lys	Leu	Asn	Ala	Lys	Met	Asn	Ile	Leu	Ile	Arg	Asp	Lys	Arg	Phe		
		610				615				620					625		
cat	tat	gat	aga	aat	aac	ata	gca	gtt	ggg	gcg	gat	gag	tca	gta	gtt	2096	
His	Tyr	Asp	Arg	Asn	Asn	Ile	Ala	Val	Gly	Ala	Asp	Glu	Ser	Val	Val		
				630					635						640		
aag	gag	gct	cat	aga	gaa	gta	att	aat	tcg	tca	aca	gag	gga	tta	ttg	2144	
Lys	Glu	Ala	His	Arg	Glu	Val	Ile	Asn	Ser	Ser	Thr	Glu	Gly	Leu	Leu		
			645					650							655		
tta	aat	att	gat	aag	gat	ata	aga	aaa	ata	tta	tca	ggt	tat	att	gta	2192	
Leu	Asn	Ile	Asp	Lys	Asp	Ile	Arg	Lys	Ile	Leu	Ser	Gly	Tyr	Ile	Val		
			660					665					670				
gaa	att	gaa	gat	act	gaa	ggg	ctt	aaa	gaa	gtt	ata	aat	gac	aga	tat	2240	
Glu	Ile	Glu	Asp	Thr	Glu	Gly	Leu	Lys	Glu	Val	Ile	Asn	Asp	Arg	Tyr		
		675					680								685		
gat	atg	ttg	aat	att	tct	agt	tta	cgg	caa	gat	gga	aaa	aca	ttt	ata	2288	
Asp	Met	Leu	Asn	Ile	Ser	Ser	Leu	Arg	Gln	Asp	Gly	Lys	Thr	Phe	Ile		
		690				695				700					705		
gat	ttt	aaa	aaa	tat	aat	gat	aaa	tta	ccg	tta	tat	ata	agt	aat	ccc	2336	
Asp	Phe	Lys	Lys	Tyr	Asn	Asp	Lys	Leu	Pro	Leu	Tyr	Ile	Ser	Asn	Pro		
				710						715					720		

aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att att 2384  
 Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile  
           725                                  730                                  735

aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa att 2432  
 Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile  
           740                                  745                                  750

tta atc ttt tct aaa aaa ggc tat gag ata gga taaggtaatt ctaggtgatt 2485  
 Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly  
           755                                  760

tttaaattat ctaaaaaaca gtaaaattaa aacatactct ttttgtaaga aatacaagga 2545  
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<211> 764

<212> PRT

<213> Bacillus anthracis

<400> 4

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                                   20                                  25                                  30  
 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu  
                                   35                                  40                                  45  
 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val  
                                   50                                  55                                  60  
 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu  
 65                                  70                                  75                                  80  
 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly  
                                   85                                  90                                  95  
 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala  
                                   100                                  105                                  110  
 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys  
                                   115                                  120                                  125  
 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln  
                                   130                                  135                                  140  
 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp  
 145                                  150                                  155                                  160  
 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser  
                                   165                                  170                                  175  
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser  
                                   180                                  185                                  190  
 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp  
                                   195                                  200                                  205  
 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp  
                                   210                                  215                                  220  
 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His  
 225                                  230                                  235                                  240  
 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser  
                                   245                                  250                                  255  
 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile  
                                   260                                  265                                  270  
 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr  
                                   275                                  280                                  285  
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu

290	295	300
Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys		
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Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala		320
	325	330
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Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly		
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Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser		
	355	360
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Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala		
	370	375
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Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr		
385	390	395
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Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys		
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Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln		
	420	425
		430
Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile		
	435	440
		445
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn		
	450	455
		460
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp		
465	470	475
		480
Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly		
	485	490
		495
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln		
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		510
Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn		
	515	520
		525
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu		
	530	535
		540
Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe		
545	550	555
		560
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile		
	565	570
		575
Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys		
	580	585
		590
Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp		
	595	600
		605
Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg		
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		620
Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val		
625	630	635
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Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu		
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Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile		
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Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg		
	675	680
		685
Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe		
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		700
Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn		
705	710	715
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Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile		
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		735
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 <212> DNA  
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 <212> DNA  
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 tcggct 66

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 Ala Val Phe Val Ser Ala  
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